

A. Harris



RAW SEQUENCE LISTING

DATE: 03/04/2002

PATENT APPLICATION: US/09/579,543

TIME: 15:38:02

Input Set : N:\Crf3\RULE60\09579543.raw

Output Set: N:\CRF3\03042002\I579543.raw

SEQUENCE LISTING

2 (1) GENERAL INFORMATION:

C--> 4 (i) APPLICANT: Gaugler, Batrice; Van den Eynde, BenoEt;
5 van der Bruggen, Pierre; Boon-Falleur, Thierry
7 (ii) TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
8 Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
10 (iii) NUMBER OF SEQUENCES: 30
12 (iv) CORRESPONDENCE ADDRESS:
13 (A) ADDRESSEE: Felfe & Lynch
14 (B) STREET: 805 Third Avenue
15 (C) CITY: New York City
16 (D) STATE: New York
17 (F) ZIP: 10022
19 (v) COMPUTER READABLE FORM:
20 (A) MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
21 (B) COMPUTER: IBM
22 (C) OPERATING SYSTEM: PC-DOS
23 (D) SOFTWARE: Wordperfect
25 (vi) CURRENT APPLICATION DATA:
C--> 26 (A) APPLICATION NUMBER: US/09/579,543
C--> 27 (B) FILING DATE: 26-May-2000
28 (C) CLASSIFICATION:
C--> 49 (vii) PRIOR APPLICATION DATA:
31 (A) APPLICATION NUMBER: 09/583,850
32 (B) FILING DATE:
34 (A) APPLICATION NUMBER: PCT/US92/04354
35 (B) FILING DATE: 22-MAY-1992
38 (A) APPLICATION NUMBER: 07/807,043
39 (B) FILING DATE: 12-DECEMBER-1991
42 (A) APPLICATION NUMBER: 07/764,365
43 (B) FILING DATE: 23-SEPTEMBER-1991
46 (A) APPLICATION NUMBER: 07/728,838
47 (B) FILING DATE: 9-JULY-1991
50 (A) APPLICATION NUMBER: 07/705,702
51 (B) FILING DATE: 23-MAY-1991
C--> 53 (viii) ATTORNEY/AGENT INFORMATION:
54 (A) NAME: Hanson, Norman D.
55 (B) REGISTRATION NUMBER: 30,946
56 (C) REFERENCE/DOCKET NUMBER: LUD 5353
C--> 58 (ix) TELECOMMUNICATION INFORMATION:
59 (A) TELEPHONE: (212) 688-9200
60 (B) TELEFAX: (212) 838-3884
C--> 64 (2) INFORMATION FOR SEQ ID NO: 1:

ENTERED

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Input Set : N:\Crif3\RULE60\09579543.raw

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65      (i) SEQUENCE CHARACTERISTICS:
66          (A) LENGTH: 462 base pairs
67          (B) TYPE: nucleic acid
68          (C) STRANDEDNESS: single
69          (D) TOPOLOGY: linear
70      (ii) MOLECULE TYPE: genomic DNA
71      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
75 ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT GAAGATCCTG      60
76 ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTTCATCCCT CAGCCAATGA GCTTACTGTT      120
77 CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG AAGTTTGTGCA AGTTCCGCCT ACAGCTCTAG      180
78 CTTGTGAATT TGTACCCTTT CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC      240
79 CCCCCTCCCA CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT      300
80 AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCTTTT GCTCTCCAG CATGCATTGT      360
81 GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG CTAGCTTGCG ACTCTACTCT      420
82 TATCTTAAct TAGCTCGGCT TCCTGCTGGT ACCCTTTGTG CC      462
C--> 86 (2) INFORMATION FOR SEQ ID NO: 2:
87      (i) SEQUENCE CHARACTERISTICS:
88          (A) LENGTH: 675 base pairs
89          (B) TYPE: nucleic acid
90          (C) STRANDEDNESS: single
91          (D) TOPOLOGY: linear
92      (ii) MOLECULE TYPE: genomic DNA
93      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
96 ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA GGT GGT      48
97 Met Ser Asp Asn Lys Lys Pro Asp Lys Ala His Ser Gly Ser Gly Gly
98      5      10      15
99 GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG TAC TCC CTG GAA      96
100 Asp Gly Asp Gly Asn Arg Cys Asn Leu Leu His Arg Tyr Ser Leu Glu
101      20      25      30
102 GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC TTC GCT GTT GTC ACA ACA      144
103 Glu Ile Leu Pro Tyr Leu Gly Trp Leu Val Phe Ala Val Val Thr Thr
104      35      40      45
105 AGT TTT CTG GCG CTC CAG ATG TTC ATA GAC GCC CTT TAT GAG GAG CAG      192
106 Ser Phe Leu Ala Leu Gln Met Phe Ile Asp Ala Leu Tyr Glu Glu Gln
107      50      55      60
108 TAT GAA AGG GAT GTG GCC TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC      240
109 Tyr Glu Arg Asp Val Ala Trp Ile Ala Arg Gln Ser Lys Arg Met Ser
110      65      70      75      80
111 TCT GTC GAT GAG GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC      288
112 Ser Val Asp Glu Asp Glu Asp Asp Glu Asp Asp Glu Asp Asp Tyr Tyr
113      85      90      95
114 GAC GAC GAG GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT      336
115 Asp Asp Glu Asp Asp Asp Asp Asp Phe Tyr Asp Asp Glu Asp Asp
116      100      105      110
117 GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA GAT GAG      384
118 Glu Glu Glu Glu Leu Glu Asn Leu Met Asp Asp Glu Ser Glu Asp Glu
119      115      120      125
120 GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA GCT GAG GAA ATG      432
121 Ala Glu Glu Glu Met Ser Val Glu Met Gly Ala Gly Ala Glu Glu Met

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122      130      135      140
123 GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT GGC CAT CAT TTA AGG AAG      480
124 Gly Ala Gly Ala Asn Cys Ala Cys Val Pro Gly His His Leu Arg Lys
125 145      150      155      160
126 AAT GAA GTG AAG TGT AGG ATG ATT TAT TTC TTC CAC GAC CCT AAT TTC      528
127 Asn Glu Val Lys Cys Arg Met Ile Tyr Phe Phe His Asp Pro Asn Phe
128      165      170      175
129 CTG GTG TCT ATA CCA GTG AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT      576
130 Leu Val Ser Ile Pro Val Asn Pro Lys Glu Gln Met Glu Cys Arg Cys
131      180      185      190
132 GAA AAT GCT GAT GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAA GAG      624
133 Glu Asn Ala Asp Glu Glu Val Ala Met Glu Glu Glu Glu Glu Glu Glu
W--> 134      195      200      210
135 GAG GAG GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT      672
136 Glu Glu Glu Glu Glu Glu Glu Glu Met Gly Asn Pro Asp Gly Phe Ser Pro
W--> 137 220      225      230      235
139 TAG      675
C--> 144 (2) INFORMATION FOR SEQ ID NO: 3:
145      (i) SEQUENCE CHARACTERISTICS:
146          (A) LENGTH: 228 base pairs
147          (B) TYPE: nucleic acid
148          (C) STRANDEDNESS: single
149          (D) TOPOLOGY: linear
150      (ii) MOLECULE TYPE: genomic DNA
151      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
154 GCATGCAGTT GCAAAGCCCA GAAGAAAGAA ATGGACAGCG GAAGAAGTGG TTGTTTTTTTT      60
155 TTCCCCTTCA TTAATTTTCT AGTTTTTAGT AATCCAGAAA ATTTGATTTT GTTCTAAAGT      120
156 TCATTATGCA AAGATGTCAC CAACAGACTT CTGACTGCAT GGTGAACCTT CATATGATAC      180
157 ATAGGATTAC ACTTGACCT GTTAAAAATA AAAGTTTGAC TTGCATAC      228
C--> 161 (2) INFORMATION FOR SEQ ID NO: 4:
162      (i) SEQUENCE CHARACTERISTICS:
163          (A) LENGTH: 1365 base pairs
164          (B) TYPE: nucleic acid
165          (C) STRANDEDNESS: single
166          (D) TOPOLOGY: linear
167      (ii) MOLECULE TYPE: genomic DNA
168      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
171 ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT      50
172 GAAGATCCTG ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT      100
173 CAGCCAATGA GCTTACTGTT CTCGTGGGGG GTTGTGAGC CTTGGGTAGG      150
174 AAGTTTTCGA AGTCCGCTT ACAGCTCTAG CTTGTGAATT TGTACCCTTT      200
175 CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCTCCCA      250
176 CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT      300
177 AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCTTT GCTCTCCCAG      350
178 CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG      400
179 CTAGCTTGCG ACTCTACTCT TATCTTAACT TAGCTCGGCT TCCTGCTGGT      450
180 ACCCTTTGTG CC      462
181 ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA      504
182 GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG      546

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Input Set : N:\Crif3\RULE60\09579543.raw

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183 TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC      588
184 TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAG ATG TTC      630
185 ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC      672
186 TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT GAG      714
187 GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC GAC GAC      756
188 GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT      798
189 GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA      840
190 GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA      882
191 GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT      924
192 GGC CAT CAT TTA AGG AAG AAT GAA GTG AAG TGT AGG ATG ATT      966
193 TAT TTC TTC CAC GAC CCT AAT TTC CTG GTG TCT ATA CCA GTG     1008
194 AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT GAA AAT GCT GAT     1050
195 GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAG GAG GAG     1092
196 GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT     1134
197 TAG                                                                1137
198 GCATGCAGTT GCAAAGCCCA GAAGAAAGAA ATGGACAGCG GAAGAAGTGG     1187
199 TTGTTTTTTTT TTCCCTTCA TTAATTTTCT AGTTTTTAGT AATCCAGAAA     1237
200 ATTTGATTTT GTTCTAAAGT TCATTATGCA AAGATGTCAC CAACAGACTT     1287
201 CTGACTGCAT GGTGAACCTT CATATGATAC ATAGGATTAC ACTTGTACCT     1337
202 GTTAAAAATA AAAGTTTGAC TTGCATAC                                  1365

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C--> 207 (2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4698 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

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217 ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT      50
218 GAAGATCCTG ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT     100
219 CAGCCAATGA GCTTACTGTT CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG     150
220 AAGTTTTGCA AGTTCGCCT ACAGCTCTAG CTTGTGAATT TGTACCCTTT     200
221 CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCTCCCA     250
222 CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT     300
223 AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCTTT GCTCTCCCAG     350
224 CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG     400
225 CTAGCTTGCG ACTCTACTCT TATCTTAACT TAGCTCGGCT TCCTGCTGGT     450
226 ACCCTTTGTG CC                                                    462
227 ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA     504
228 GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG     546
229 TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC     588
230 TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAG ATG TTC     630
231 ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC     672
232 TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT GAG     714
233 GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC GAC GAC     756
234 GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT     798
235 GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA     840
236 GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA     882
237 GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC T                    916

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/579,543

DATE: 03/04/2002

TIME: 15:38:03

Input Set : N:\Crif3\RULE60\09579543.raw

Output Set: N:\CRF3\03042002\I579543.raw

L:4 M:220 C: Keyword misspelled or invalid format, [(i) APPLICANT:]
L:26 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:27 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:37 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:41 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:45 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:49 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:53 M:220 C: Keyword misspelled or invalid format, [(viii) ATTORNEY/AGENT INFORMATION:]
L:58 M:220 C: Keyword misspelled or invalid format, [(ix) TELECOMMUNICATION INFORMATION:]
L:64 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:86 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:134 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:137 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:144 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:161 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
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L:394 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
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L:635 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:665 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:710 M:111 C: (47) String data converted to upper case,
L:719 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:734 M:111 C: (47) String data converted to upper case,
M:111 Repeated in SeqNo=12
L:756 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:827 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:899 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:939 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:1002 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:1067 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
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L:1496 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]



Creation date: 02-04-2004
Indexing Officer: SCHASE1 - SUSAN CHASE
Team: OIPEBackFileIndexing
Dossier: 09579543

Legal Date: 03-18-2002

No.	Doccode	Number of pages
1	CTRS	6

Total number of pages: 6

Remarks:

Order of re-scan issued on